

In the Claims

Please replace all prior versions, and listings, of claims in the application with the following list of claims:

1. (Currently Amended) A method for identifying at least one human coding region/gene, including mutated or polymorphic variants thereof, which is associated with a bipolar disorder, comprising:

identifying the position of a coding region/gene in an 8.9 cM region of human chromosome 18q disposed between polymorphic markers D18S68 and D18S979 or a fragment thereof ~~in a that can be compared to an equivalent region of DNA from a person afflicted with a bipolar disorder~~, and

detecting differences between the coding region/gene in the DNA of the 8.9 cM region of human chromosome 18q disposed between polymorphic markers D18S68 and D18S979 or a fragment thereof one or more control individuals and the coding region/gene equivalent region in the DNA of an individual afflicted with the a bipolar disorder, wherein a difference in the coding region/gene in the DNA of the one or more control individuals and the coding region/gene in the DNA of the individual afflicted with the bipolar disorder equivalent region identifies the coding region/gene or mutated or polymorphic variant thereof as associated with the bipolar disorder.

2. (Currently Amended) A method for identifying at least one human coding region/gene, including mutated or polymorphic variants thereof, which is associated with a bipolar disorder, comprising:

identifying the position of a control coding region/gene in a YAC clone comprising a portion of human chromosome 18q disposed between polymorphic markers D18S60 and D18S61 ~~that can be compared to an equivalent region of DNA from a person afflicted with the a bipolar disorder~~, and

detecting differences between the control coding region/gene of the YAC clone comprising a portion of human chromosome 18q disposed between polymorphic markers D18S60 and D18S61 and the coding region/gene equivalent region of DNA of an individual

afflicted with the a bipolar disorder, wherein a difference in the control coding region/gene and the coding region/gene of DNA of the individual afflicted with a bipolar disorder equivalent ~~region of DNA~~ identifies that the coding region/gene or mutated or polymorphic variant thereof is associated with the bipolar disorder.

3. (Previously Presented) The method of claim 2 wherein said portion comprises the region of chromosome 18q between polymorphic markers D18S68 and D18S979 or a fragment of said region.

4. (Previously Presented) The method of claim 2 wherein said YAC clone is 961_h_9, 942_c_3, 766_f_12, 731_c_7, 907_e_1, 752_g_8 or 717_d_3.

5. (Previously Presented) The method of claim 4 wherein said YAC clone is 961_h_9, 766_f_12 or 907_e_1.

6-47. (Cancelled)